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0460  
02/27/01  
OIPE

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/754,949

DATE: 01/25/2001

TIME: 11:12:45

Input Set : A:\SCIOS.012Aseqlist.txt

Output Set: N:\CRF3\01252001\I754949.raw

ENTERED

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4 <110> APPLICANT: MCCARTHY, JUSTIN
5   CORDELL, BARBARA
7 <120> TITLE OF INVENTION: METHODS FOR IDENTIFYING INHIBITORS OF
8   NEURONAL DEGENERATION
10 <130> FILE REFERENCE: SCIOS.012A
C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/754,949
C--> 12 <141> CURRENT FILING DATE: 2001-01-04
12 <160> NUMBER OF SEQ ID NOS: 16
14 <170> SOFTWARE: FastSEQ for Windows Version 4.0
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17 <211> LENGTH: 942
18 <212> TYPE: DNA
19 <213> ORGANISM: Homo Sapien
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23 gctgggaagc ccccgcggg ggctctgggc accccggcgg ccgccgctgc caacgagctc 120
24 aacaacaacc tcccgggcgg cgcgccggcc gcacctgccg tccccgggtcc cgggggcggtg 180
25 aactgcgcgg tcggctccgc catgctgacg cgggcgcccc cggcccgcgg cccgcggcgg 240
26 tcggaggacg agccccagc cgctctgcc tcggctgcac cgccgcccc gcgtagacgag 300
27 gaggagccgg acggcgctcc agagaagggc aagagctcgg gccccagtg caggaaaggc 360
28 aaggggcaga tcgagaagag gaagctgcgg gagaagcggc gctccaccgg cgtgggtcaac 420
29 atccctgccg cagagtgtt agatgagtag gaagatgatg aagcagggca gaaagagcgg 480
30 aaacgagaag atgcaattac acaacagAAC actattcaga atgaagctgt aaacttacta 540
31 gatccaggca gttcctatct gctacaggag ccacctagaa cagtttcagg cagatataaa 600
32 agcacaacca gtgtctctga agaagatgtc tcaagtagat attctcgaac agatagaagt 660
33 gggttcccta gatataacag ggatgcaaat gtttcaggta ctctggtttc aagtagcaca 720
34 ctggaaaaga aaattgaaga tcttgaaaag gaagtagtaa cagaaagaca agaaaacct 780
35 agacttgtag gactgatgca agataaagag gaaatgattg gaaaactcaa agaagaaatt 840
36 gatttattaa atagagacct agatgacata gaagatgaaa atgaacagct aaagcaggaa 900
37 aataaaaactc ttttgaaagt tgtgggtcag ctgaccaggt ag 942
39 <210> SEQ ID NO: 2
40 <211> LENGTH: 341
41 <212> TYPE: PRT
42 <213> ORGANISM: Homo Sapien
44 <400> SEQUENCE: 2
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46 1 5 10 15
47 Asp Trp Lys Ala Lys Arg Lys Met Arg Ala Lys Asn Gly Ala Gly Gly
48 20 25 30
49 Gly Ser Ser Asp Ala Ala Gly Lys Ala Gly Ala Gly Thr Ala Ala Ala
50 35 40 45
51 Ala Ala Asn Asn Asn Asn Gly Gly Ala Ala Ala Ala Val Gly Gly Gly
52 50 55 60
53 Val Asn Cys Ala Val Gly Ser Ala Met Thr Arg Ala Ala Arg Gly Arg
54 65 70 75 80
55 Arg Ser Asp Ala Ala Ser Ala Ser Ala Ala Arg Asp Asp Gly Val Lys
56 85 90 95

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57 Gly Lys Ser Ser Gly Ser Ala Arg Lys Gly Lys Gly Lys Arg Lys Arg  
 58                   100                   105                   110  
 59 Lys Arg Arg Ser Thr Gly Val Val Asn Ala Ala Cys Asp Tyr Asp Asp  
 60                   115                   120                   125  
 61 Ala Gly Lys Arg Lys Arg Asp Ala Thr Asn Thr Asn Ala Val Asn Asp  
 62                   130                   135                   140  
 63 Gly Ser Ser Tyr Arg Thr Val Ser Gly Arg Tyr Lys Ser Thr Thr Ser  
 64 145                   150                   155                   160  
 65 Val Ser Asp Val Ser Ser Arg Tyr Ser Arg Thr Asp Arg Ser Gly Arg  
 66                   165                   170                   175  
 67 Tyr Asn Arg Asp Ala Asn Val Ser Gly Thr Val Ser Ser Ser Thr Lys  
 68                   180                   185                   190  
 69 Lys Asp Lys Val Val Thr Arg Asn Arg Val Arg Met Asp Lys Met Gly  
 70                   195                   200                   205  
 71 Lys Lys Asp Asn Arg Asp Asp Asp Asn Lys Asn Lys Thr Lys Val  
 72                   210                   215                   220  
 73 Val Gly Thr Arg Met Ala Thr Gly Gly Tyr Arg Thr Ser Ser Gly Gly  
 74 225                   230                   235                   240  
 75 Gly Ser Thr Thr Asp Trp Lys Ala Lys Arg Lys Met Arg Ala Lys Asn  
 76                   245                   250                   255  
 77 Gly Ala Gly Gly Gly Ser Ser Asp Ala Ala Gly Lys Ala Gly Ala Gly  
 78                   260                   265                   270  
 79 Thr Ala Ala Ala Ala Ala Asn Asn Asn Asn Gly Gly Ala Ala Ala Ala  
 80                   275                   280                   285  
 81 Val Gly Gly Gly Val Asn Cys Ala Val Gly Ser Ala Met Thr Arg Ala  
 82                   290                   295                   300  
 83 Ala Arg Gly Arg Arg Asp Ala Ala Ser Ala Ser Ala Ala Arg Asp Asp  
 84 305                   310                   315                   320  
 85 Gly Val Lys Gly Lys Ser Ser Gly Ser Ala Arg Lys Gly Lys Gly Lys  
 86                   325                   330                   335  
 87 Arg Lys Arg Lys Arg  
 88                   340

91 &lt;210&gt; SEQ ID NO: 3

92 &lt;211&gt; LENGTH: 1404

93 &lt;212&gt; TYPE: DNA

94 &lt;213&gt; ORGANISM: Homo Sapien

96 &lt;400&gt; SEQUENCE: 3

97 atgacagagt tacctgcacc gttgtcctac ttccagaatg cacagatgtc tgaggacaac 60  
 98 cacctgagca atactgtacg tagccagaat gacaatagag aacggcagga gcacaacgac 120  
 99 agacggagcc ttggccaccc tgagccatta tctaattggac gaccccaggg taactcccgg 180  
 100 caggtggtgg agcaagatga ggaagaagat gaggagctga cattgaaata tggcgccaag 240  
 101 catgtgatca tgctctttgt ccctgtgact ctctgcatgg tgggtggtcgt ggctaccatt 300  
 102 aagtcagtca gcttttatac ccggaaggat gggcagctaa tctatacccc attcacagaa 360  
 103 gataccgaga ctgtgggcca gagagccctg cactcaattc tgaatgctgc catcatgac 420  
 104 agtgtcattg ttgtcatgac tatcctcctg gtgggtctgt ataaatacag gtgctataag 480  
 105 gtcattccatg cctggcttat tatatcatct ctattgttgc tgttcttttt ttcatlcatt 540  
 106 tacttggggg aagtgtttaa aacctataac gttgctgtgg actacattac tgttgcactc 600  
 107 ctgactgga attttggtgt ggtgggaatg atttccattc actggaaagg tccacttcga 660  
 108 ctccagcagg catatctcat tatgattagt gccctcatgg ccctggtgtt tatcaagtac 720

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109 ctccctgaat ggactgcgtg gotcatcttg gctgtgattt cagtatatga tttagtggct 780
110 gttttgtgtc cgaaagggtc acttcgtatg ctgggtgaaa cagctcagga gagaaatgaa 840
111 acgctttttc cagctctcat ttactcttca acaatgggtg ggttggtgaa tatggcagaa 900
112 ggagacccgg aagctcaaag gagagtatcc aaaaattcca agtataatgc agaaagcaca 960
113 gaaagggagt cacaagacac tgttgacagag aatgatgatg gcggggttcag tgaggaatgg 1020
114 gaagcccaga gggacagtca tctagggcct catcgtctta cacctgagtc acgagctgct 1080
115 gtccaggaac ttccagcag tctctcgct ggtgaagacc cagaggaaaag gggagtaaaa 1140
116 cttggattgg gagatttcat tttctacagt gttctggttg gtaaagcctc agcaacagcc 1200
117 agtggagact ggaacacaaac catagcctgt ttctagcca tattaattgg tttgtgcctt 1260
118 acattattac tccttgccat ttccaagaaa gcattgccag ctcttccaat ctccatcacc 1320
119 tttgggcttg ttttctactt tgccacagat tatcttgtag agccttttat ggaccaatta 1380
120 gcattccatc aattttatat ctag 1404

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122 &lt;210&gt; SEQ ID NO: 4

123 &lt;211&gt; LENGTH: 467

124 &lt;212&gt; TYPE: PRT

125 &lt;213&gt; ORGANISM: Homo Sapien

127 &lt;400&gt; SEQUENCE: 4

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128 Met Thr Glu Leu Pro Ala Pro Leu Ser Tyr Phe Gln Asn Ala Gln Met
129 1 5 10 15
130 Ser Glu Asp Asn His Leu Ser Asn Thr Val Arg Ser Gln Asn Asp Asn
131 20 25 30
132 Arg Glu Arg Gln Glu His Asn Asp Arg Arg Ser Leu Gly His Pro Glu
133 35 40 45
134 Pro Leu Ser Asn Gly Arg Pro Gln Gly Asn Ser Arg Gln Val Val Glu
135 50 55 60
136 Gln Asp Glu Glu Glu Asp Glu Glu Leu Thr Leu Lys Tyr Gly Ala Lys
137 65 70 75 80
138 His Val Ile Met Leu Phe Val Pro Val Thr Leu Cys Met Val Val Val
139 85 90 95
140 Val Ala Thr Ile Lys Ser Val Ser Phe Tyr Thr Arg Lys Asp Gly Gln
141 100 105 110
142 Leu Ile Tyr Thr Pro Phe Thr Glu Asp Thr Glu Thr Val Gly Gln Arg
143 115 120 125
144 Ala Leu His Ser Ile Leu Asn Ala Ala Ile Met Ile Ser Val Ile Val
145 130 135 140
146 Val Met Thr Ile Leu Leu Val Val Leu Tyr Lys Tyr Arg Cys Tyr Lys
147 145 150 155 160
148 Val Ile His Ala Trp Leu Ile Ile Ser Ser Leu Leu Leu Leu Phe Phe
149 165 170 175
150 Phe Ser Phe Ile Tyr Leu Gly Glu Val Phe Lys Thr Tyr Asn Val Ala
151 180 185 190
152 Val Asp Tyr Ile Thr Val Ala Leu Leu Ile Trp Asn Phe Gly Val Val
153 195 200 205
154 Gly Met Ile Ser Ile His Trp Lys Gly Pro Leu Arg Leu Gln Gln Ala
155 210 215 220
156 Tyr Leu Ile Met Ile Ser Ala Leu Met Ala Leu Val Phe Ile Lys Tyr
157 225 230 235 240
158 Leu Pro Glu Trp Thr Ala Trp Leu Ile Leu Ala Val Ile Ser Val Tyr
159 245 250 255

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160 Asp Leu Val Ala Val Leu Cys Pro Lys Gly Pro Leu Arg Met Leu Val
161      260      265      270
162 Glu Thr Ala Gln Glu Arg Asn Glu Thr Leu Phe Pro Ala Leu Ile Tyr
163      275      280      285
164 Ser Ser Thr Met Val Trp Leu Val Asn Met Ala Glu Gly Asp Pro Glu
165      290      295      300
166 Ala Gln Arg Arg Val Ser Lys Asn Ser Lys Tyr Asn Ala Glu Ser Thr
167 305      310      315      320
168 Glu Arg Glu Ser Gln Asp Thr Val Ala Glu Asn Asp Asp Gly Gly Phe
169      325      330      335
170 Ser Glu Glu Trp Glu Ala Gln Arg Asp Ser His Leu Gly Pro His Arg
171      340      345      350
172 Ser Thr Pro Glu Ser Arg Ala Ala Val Gln Glu Leu Ser Ser Ser Ile
173      355      360      365
174 Leu Ala Gly Glu Asp Pro Glu Glu Arg Gly Val Lys Leu Gly Leu Gly
175      370      375      380
176 Asp Phe Ile Phe Tyr Ser Val Leu Val Gly Lys Ala Ser Ala Thr Ala
177 385      390      395      400
178 Ser Gly Asp Trp Asn Thr Thr Ile Ala Cys Phe Val Ala Ile Leu Ile
179      405      410      415
180 Gly Leu Cys Leu Thr Leu Leu Leu Leu Ala Ile Phe Lys Lys Ala Leu
181      420      425      430
182 Pro Ala Leu Pro Ile Ser Ile Thr Phe Gly Leu Val Phe Tyr Phe Ala
183      435      440      445
184 Thr Asp Tyr Leu Val Gln Pro Phe Met Asp Gln Leu Ala Phe His Gln
185      450      455      460
186 Phe Tyr Ile
187 465
190 <210> SEQ ID NO: 5
191 <211> LENGTH: 1346
192 <212> TYPE: DNA
193 <213> ORGANISM: Homo Sapien
195 <400> SEQUENCE: 5
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197 atgtcggccg agagccccac gccgcgtcc tgccaggagg gcaggcaggg cccagaggat 120
198 ggagagaaca ctgcccagtg gagaagccag gagaacgagg aggacggtga ggaggacct 180
199 gaccgctatg tctgtagtgg ggttccccgg cggccgccag gcctggagga agagctgacc 240
200 ctcaaatacg gagcgaagca cgtgatcatg ctgtttgtgc ctgtcactct gtgcatgac 300
201 gtggtggtag ccaccatcaa gtctgtgcgc ttctacacag agaagaatgg acagctcatc 360
202 tacacgacat tctactgagga cacaccctcg gtgggccagc gcctcctcaa ctccgtgctg 420
203 aacaccctca tcatgatcag cgtcatcgtg gttatgacca tcttcttggg ggtgctctac 480
204 aagtaccgct gctacaagtt catccatggc tggttgatca tgtcttctact gatgctgctg 540
205 ttctctctca cctatatcta ccttggggaa gtgctcaaga cctacaatgt ggccatggac 600
206 taccacaccc tcttgctgac tgtctggaac ttccggggcag tgggcatggg gtgcatccac 660
207 tggaagggcc ctctggtgct gcagcaggcc tacctcatca tgatcagtgc gctcatggcc 720
208 ctagtgttca tcaagtacct cccagagtgg tccgcgtggg tcatcctggg cgccatctct 780
209 gtgtatgatc tcgtggctgt gctgtgtccc aaagggcctc tgagaatgct ggtagaaact 840
210 gcccaggaga gaaatgagcc catattccct gccctgatat actcatctgc catggtgtgg 900
211 acggttgcca tggcgaagct ggaccctcc tctcagggtg cctccagct cccctacgac 960

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Input Set : A:\SCIOS.012Aseqlist.txt

Output Set: N:\CRF3\01252001\I754949.raw

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212 ccggagatgg aagaagactc ctatgacagt tttgggggagc cttcataccc cgaagtcttt 1020
213 gaggctccct tgactggcta cccaggggag ggctggagga agaggaggaa aggggcgtga 1080
214 agcttggcct cggggacttc atcttctaca gtgtgctggg gggcaaggcg gctgccacgg 1140
215 gcagcgggga ctggaatacc acgctggcct gcttcgtggc catcctcatt ggcttgtgtc 1200
216 tgaccctcct gctgcttgct gtgttcaaga aggcgctgcc cgccctcccc atctccatca 1260
217 cgttcgggct catcttttac ttctccacgg acaacctggg gcggccgttc atggacaccc 1320
218 tggcctccca tcagctctac atctga 1346
220 <210> SEQ ID NO: 6
221 <211> LENGTH: 448
222 <212> TYPE: PRT
223 <213> ORGANISM: Homo Sapien
225 <400> SEQUENCE: 6
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227 1 5 10 15
228 Arg Thr Ser Leu Met Ser Ala Glu Ser Pro Thr Pro Arg Ser Cys Gln
229 20 25 30
230 Glu Gly Arg Gln Gly Pro Glu Asp Gly Glu Asn Thr Ala Gln Trp Arg
231 35 40 45
232 Ser Gln Glu Asn Glu Glu Asp Gly Glu Glu Asp Pro Asp Arg Tyr Val
233 50 55 60
234 Cys Ser Gly Val Pro Gly Arg Pro Pro Gly Leu Glu Glu Glu Leu Thr
235 65 70 75 80
236 Leu Lys Tyr Gly Ala Lys His Val Ile Met Leu Phe Val Pro Val Thr
237 85 90 95
238 Leu Cys Met Ile Val Val Val Ala Thr Ile Lys Ser Val Arg Phe Tyr
239 100 105 110
240 Thr Glu Lys Asn Gly Gln Leu Ile Tyr Thr Thr Phe Thr Glu Asp Thr
241 115 120 125
242 Pro Ser Val Gly Gln Arg Leu Leu Asn Ser Val Leu Asn Thr Leu Ile
243 130 135 140
244 Met Ile Ser Val Ile Val Val Met Thr Ile Phe Leu Val Val Leu Tyr
245 145 150 155 160
246 Lys Tyr Arg Cys Tyr Lys Phe Ile His Gly Trp Leu Ile Met Ser Ser
247 165 170 175
248 Leu Met Leu Leu Phe Leu Phe Thr Tyr Ile Tyr Leu Gly Glu Val Leu
249 180 185 190
250 Lys Thr Tyr Asn Val Ala Met Asp Tyr Pro Thr Leu Leu Leu Thr Val
251 195 200 205
252 Trp Asn Phe Gly Ala Val Gly Met Val Cys Ile His Trp Lys Gly Pro
253 210 215 220
254 Leu Val Leu Gln Gln Ala Tyr Leu Ile Met Ile Ser Ala Leu Met Ala
255 225 230 235 240
256 Leu Val Phe Ile Lys Tyr Leu Pro Glu Trp Ser Ala Trp Val Ile Leu
257 245 250 255
258 Gly Ala Ile Ser Val Tyr Asp Leu Val Ala Val Leu Cys Pro Lys Gly
259 260 265 270
260 Pro Leu Arg Met Leu Val Glu Thr Ala Gln Glu Arg Asn Glu Pro Ile
261 275 280 285
262 Phe Pro Ala Leu Ile Tyr Ser Ser Ala Met Val Trp Thr Val Gly Met

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/754,949

DATE: 01/25/2001

TIME: 11:12:46

Input Set : A:\SCIOS.012Aseqlist.txt

Output Set: N:\CRF3\01252001\I754949.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application No

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date